```
        0                    20                    40
        .                    .                     .
GAAAATGGCGCCTCACGGCCCGGGTAGTCTTACGACCCTGGTGCCCTGGGCTGCCGCCCT
---+---------+---------+---------+---------+---------+------
CTTTTACCGCGGAGTGCCGGGCCCATCAGAATGCTGGGACCACGGGACCCGACGGCGGGA
    M  A  P  H  G  P  G  S  L  T  T  L  V  P  W  A  A  A  L
                                 ‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾

        60                   80                    100
        .                    .                     .
GCTCCTCGCTCTGGGCGTGGAAAGGGCTCTGGCGCTACCCGAGATATGCACCCAATGTCC
---+---------+---------+---------+---------+---------+------
CGAGGAGCGAGACCCGCACCTTTCCCGAGACCGCGATGGGCTCTATACGTGGGTTACAGG
   L  L  A  L  G  V  E  R  A  L  A  L  P  E  I  C  T  Q  C  P
   ‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾

        120                  140                   160
        .                    .                     .
AGGGAGCGTGCAAAATTTGTCAAAGTGGCCTTTTATTGTAAAACGACACGAGAGCTAAT
---+---------+---------+---------+---------+---------+------
TCCCTCGCACGTTTTAAACAGTTTTCACCGGAAAATAACATTTTGCTGTGCTCTCGATTA
   G  S  V  Q  N  L  S  K  V  A  F  Y  C  K  T  T  R  E  L  M

        180                  200                   220
        .                    .                     .
GCTGCATGCCCGTTGCTGCCTGAATCAGAAGGGCACCATCTTGGGGCTGGATCTCCAGAA
---+---------+---------+---------+---------+---------+------
CGACGTACGGGCAACGACGGACTTAGTCTTCCCGTGGTAGAACCCCGACCTAGAGGTCTT
   L  H  A  R  C  C  L  N  Q  K  G  T  I  L  G  L  D  L  Q  N

        240                  260                   280
        .                    .                     .
CTGTTCTCTGGAGGACCCTGGTCCAAACTTTCATCAGGCACATACCACTGTCATCATAGA
---+---------+---------+---------+---------+---------+------
GACAAGAGACCTCCTGGGACCAGGTTTGAAAGTAGTCCGTGTATGGTGACAGTAGTATCT
   C  S  L  E  D  P  G  P  N  F  H  Q  A  H  T  T  V  I  I  D

        300                  320                   340
        .                    .                     .
CCTGCAAGCAAACCCCCTCAAAGGTGACTTGGCCAACACCTTCCGTGGCTTTACTCAGCT
---+---------+---------+---------+---------+---------+------
GGACGTTCGTTTGGGGGAGTTTCCACTGAACCGGTTGTGGAAGGCACCGAAATGAGTCGA
   L  Q  A  N  P  L  K  G  D  L  A  N  T  F  R  G  F  T  Q  L
```

FIG. 1A

```
        360                    380                    400
          .                      .                      .
CCAGACTCTGATACTGCCACAACATGTCAACTGTCCTGGAGGAATTAATGCCTGGAATAC
---+---------+---------+---------+---------+---------+------
GGTCTGAGACTATGACGGTGTTGTACAGTTGACAGGACCTCCTTAATTACGGACCTTATG
 Q  T  L  I  L  P  Q  H  V  N  C  P  G  G  I  N  A  W  N  T

        420                    440                    460
          .                      .                      .
TATCACCTCTTATATAGACAACCAAATCTGTCAAGGGCAAAAGAACCTTTGCAATAACAC
---+---------+---------+---------+---------+---------+------
ATAGTGGAGAATATATCTGTTGGTTTAGACAGTTCCCGTTTTCTTGGAAACGTTATTGTG
 I  T  S  Y  I  D  N  Q  I  C  Q  G  Q  K  N  L  C  N  N  T

        480                    500                    520
          .                      .                      .
TGGGGACCCAGAAATGTGTCCTGAGAATGGATCTTGTGTACCTGATGGTCCAGGTCTTTT
---+---------+---------+---------+---------+---------+------
ACCCCTGGGTCTTTACACAGGACTCTTACCTAGAACACATGGACTACCAGGTCCAGAAAA
 G  D  P  E  M  C  P  E  N  G  S  C  V  P  D  G  P  G  L  L

        540                    560                    580
          .                      .                      .
GCAGTGTGTTTGTGCTGATGGTTTCCATGGATACAAGTGTATGCGCCAGGGCTCGTTCTC
---+---------+---------+---------+---------+---------+------
CGTCACACAAACACGACTACCAAAGGTACCTATGTTCACATACGCGGTCCCGAGCAAGAG
 Q  C  V  C  A  D  G  F  H  G  Y  K  C  M  R  Q  G  S  F  S

        600                    620                    640
          .                      .                      .
ACTGCTTATGTTCTTCGGGATTCTGGGAGCCACCACTCTATCCGTCTCCATTCTGCTTTG
---+---------+---------+---------+---------+---------+------
TGACGAATACAAGAAGCCCTAAGACCCTCGGTGGTGAGATAGGCAGAGGTAAGACGAAAC
 L  L  M  F  F  G  I  L  G  A  T  T  L  S  V  S  I  L  L  W

        660                    680                    700
          .                      .                      .
GGCGACCCAGCGCCGAAAAGCCAAGACTTCATGAACTACATAGGTCTTACCATTGACCTA
---+---------+---------+---------+---------+---------+------
CCGCTGGGTCGCGGCTTTTCGGTTCTGAAGTACTTGATGTATCCAGAATGGTAACTGGAT
 A  T  Q  R  R  K  A  K  T  S  *
```

FIG. 1B

```
      720                   740                   760
       .         .          .         .          .         .
AGATCAATCTGAACTATCTTAGCCCAGTCAGGGAGCTCTGCTTCCTAGAAAGGCATCTTT
---+---------+---------+---------+---------+---------+------
TCTAGTTAGACTTGATAGAATCGGGTCAGTCCCTCGAGACGAAGGATCTTTCCGTAGAAA


      780                   800                   820
       .         .          .         .          .         .
CGCCAGTGGATTCGCCTCAAGGTTGAGGCCGCCATTGGAAGATGAAAAATTGCACTCCCT
---+---------+---------+---------+---------+---------+------
GCGGTCACCTAAGCGGAGTTCCAACTCCGGCGGTAACCTTCTACTTTTTAACGTGAGGGA


      840                   860                   880
       .         .          .         .          .         .
TGGTGTAGACAAATACCAGTTCCCATTGGTGTTGTTGCCTATAATAAACACTTTTTTCTT
---+---------+---------+---------+---------+---------+------
ACCACATCTGTTTATGGTCAAGGGTAACCACAACAACGGATATTATTTGTGAAAAAGAA


      900
       .         .
TTTTAAAAAAAAAAAAAAAAAAAA
---+---------+---------
AAAATTTTTTTTTTTTTTTTTTTT
```

FIG. 1C

Human TGFα   VVSHFNDCPDSHTQF-CFH-GTCRFLVQEDKPACVCHSGYVGARCEHADLLA

TGFα-HIII   GQKNLCNNTGDPEMCPENGSCVPDGPGLLQ-CVCADGFHGYKCMRQGSFSLLM

FIG. 2